AMENDMENTS TO THE SPECIFICATION UNDER 37 C.F.R. § 1.121(b)(1)

1. Please amend the paragraph after the heading CROSS REFERENCE TO RELATED APPLICATIONS as follows:

This application is a divisional application of U.S. Patent Application Ser. No. 09/640,363, filed August 16, 2000, which claims priority to U.S. Provisional Application Serial Nos. 60/149,115, filed August 16, 1999,1999; 60/172,452, filed December 17, 1999; 60/176,570, filed January 18, 2000; and 60/194,534, filed April 4, 2000.

2. Please amend the paragraphs beginning on page 8, line 4 and ending on line 14, as follows:

Active site I:

35 AA's upstreamdownstream from N-terminus: STTK (SEQ ID NO:1)

Active site II:

57 AA's upstreamdownstream from STTK (SEQ ID NO:1) motif: SGC, SGN,

Active site III:

111 AA's upstreamdownstream from SGC motif: KTG

Active site IV:

41 AA's upstream from SGC motif: ENKD (SEQ ID NO:2)

3. Please amend the paragraphs beginning on page 8, line 30 and continuing through page 9, line 8, as follows:

Active site I:

PBP: 35 AA's <u>upstreamdownsteam</u> from N-terminus: STTK (SEQ ID NO:1) NAALADase: 38 AA's <u>upstreamdownstream</u> from N-terminus: STQK (SEQ

<u>ID NO:3)</u>

or SAN

Active site II:

PBP: 57 AA's upstreamdownstream from STTK (SEQ ID NO:1) motif: SGC,

SGN, or SAN

NAALADase: 59 AA's upstreamdownstream from STQK (SEQ ID NO:3)

motif: SFG

Active site III:

PBP: 111 AA's upstreamdownstream from SGC motif: KTG

	Active site III: PBP: 111 AA's upstreamdownstream from SGC motif: KTG NAALADase: 110 AA's upstreamdownstream from SFG motif: KLG				
	Active site IV: PBP: 41 AA's upstreamdowns NAALADase: 41 AA's upstream	tream from SGC motif: ENKD (SEQ ID NO:2) mdownstream from SFG motif: ERGV (SEQ			
<u>ID NO:4)</u>					
	4. Please amend the parag	graphs on beginning on page 9, line 34 and			
continuing through page 13, line 2, as follows:					
<u>ID NO:1)</u>	Active site I: PBP: 35 AA's upstreamdowns	tream from N-terminus: STTK_(SEQ			
	NAALADase: 38 AA's upstreamdownstream from N-terminus: STQK (SEQ				
<u>ID NO:3)</u>	>dbj AP001769:	NSRK (SEQ ID NO:5)			
motif:motif: SFG	Active site II: PBP: 57 AA's upstreamdownstream from STTK (SEQ ID NO:1) SGC, SGN, or SAN NAALADase: 59 AA's upstreamdownstream from STQK (SEQ ID NO:3)				
	>dbj AP001769:	SFG			
	Active site III: PBP:111 AA's upstreamdowns NAALADase: 110 AA's upstre >dbj AP001769:	stream from SGC motif:KTG eamdownstream from SFG motif: KLG KLG			
<u>ID NO:2)</u> <u>ID NO:4)</u>	Active site IV: PBP:41 AA's upstream downst	ream from SGC motif: ENKD (SEQ			
	NAALADase: 41 AA's upstrea	mdownstream from SFG motif: ERGV (SEQ			
	>dbj AP001769: 2) >dbj AP000827.2 AP000827	ERSI (SEQ ID NO:6) Homo sapiens chromosome 11 clone RP.			
ID NO.1)	Active site I: PBP: 35 AA's upstreamdownst	ream from N-terminus: STTK_(SEQ			
<u>ID NO:1)</u>	NAALADase: 38 AA's upstrea	mdownstream from N-terminus: STQK (SEQ			
<u>ID NO:3)</u>	>dbj AP000827.2:	NSRK (SEQ ID NO:5)			

Active site II:

	PBP: 57 AA's upstreamdownstream from SGC, SGN, or SAN NAALADase: 59 AA's upstream downs	
motif: SFG	>dbj AP000827.2:	SFG
	Active site III: PBP:111 AA's upstreamdownstream fron NAALADase: 110 AA's upstreamdown >dbj AP000827.2:	om SGC motif: KTG astream from SFG motif: KLG KLG
ID NO:2)	Active site IV: PBP:41 AA's upstreamdownstream from	m SGC motif: ENKD (SEQ
<u>ID NO:4)</u>	NAALADase: 41 AA's upstreamdowns	stream from SFG motif: ERGV (SEQ
<u> </u>	>dbj AP000827.2: 3) >dbj AP000648.2 AP000648 Homo	ERSI (SEQ ID NO:6) sapiens chromosome 11 clone CM.
<u>ID NO:1)</u>	Active site I: PBP: 35 AA's upstreamdownstream fro	m N-terminus: STTK_(SEQ
ID NO:3)	NAALADase: 38 AA's upstreamdowns	tream from N-terminus: STQK (SEQ
	11 11 4 7000 6 40 0	NODE (CDC to to c)
	>>dbj AP000648.2:	NSRK (SEQ ID NO:5)
	>>dbj AP000648.2: Active site II: PBP: 57 AA's upstreamdownstream from SGC, SGN, or SAN NAALADase: 59 AA's upstreamdowns	m STTK (SEQ ID NO:1)
motif: motif: SFG	Active site II: PBP: 57 AA's upstream downstream from SGC, SGN, or SAN	m STTK (SEQ ID NO:1)
	Active site II: PBP: 57 AA's upstreamdownstream from SGC, SGN, or SAN NAALADase: 59 AA's upstreamdowns	m STTK (SEQ ID NO:1) tream from STQK (SEQ ID NO:3) SFG om SGC motif:
	Active site II: PBP: 57 AA's upstreamdownstream from SGC, SGN, or SAN NAALADase: 59 AA's upstreamdowns >dbj AP000648.2: Active site III: PBP:111 AA's upstreamdownstream from NAALADase: 110 AA's upstreamdown	m STTK (SEQ ID NO:1) tream from STQK (SEQ ID NO:3) SFG om SGC motif:
motif: SFG	Active site II: PBP: 57 AA's upstreamdownstream from SGC, SGN, or SAN NAALADase: 59 AA's upstreamdowns >dbj AP000648.2: Active site III: PBP:111 AA's upstreamdownstream from NAALADase: 110 AA's upstreamdown >dbj AP000648.2: Active site IV: PBP:41 AA's upstreamdownstream from NAALADase: 41 AA's upstreamdownstream from NAALADase: 41 AA's upstreamdownstream	m STTK (SEQ ID NO:1) tream from STQK (SEQ ID NO:3) SFG om SGC motif:
motif: SFG ID NO:2)	Active site II: PBP: 57 AA's upstreamdownstream from SGC, SGN, or SAN NAALADase: 59 AA's upstreamdowns >dbj AP000648.2: Active site III: PBP:111 AA's upstreamdownstream from NAALADase: 110 AA's upstreamdown >dbj AP000648.2: Active site IV: PBP:41 AA's upstreamdownstream from PBP:41 AA's upstreamdownstre	tream from STQK (SEQ ID NO:3) SFG om SGC motif:

<u>ID NO:1)</u>	PBP: 35 AA's upstreamdownstream from N-term	ninus:	. STTK_(SEQ
<u>ID NO:3)</u>	NAALADase: 38 AA's upstreamdownstream fro	m N-terminus	s: STQK <u>(SEQ</u>
	gb AC074003.2 AC074003:	STQ-	
	Active site II: PBP: 57 AA's upstreamdownstream from STTK SGC, SGN, or SAN NAALADase: 59 AA's upstreamdownstream fro gb AC074003.2 AC074003:		
	Active site III: PBP:111 AA's upstreamdownstream from SGC r NAALADase: 110 AA's upstreamdownstream from gb AC074003.2 AC074003:	motif:	
<u>ID NO:2)</u> <u>ID NO:4)</u>	Active site IV: PBP:41 AA's upstreamdownstream from SGC motif: ENKD (SEQ		
	NAALADase: 41 AA's upstreamdownstream from	m SFG motif:	ERGV <u>(SEQ</u>
	gb AC074003.2 AC074003 5)> emb AL162372.6 AL162372 Homo sapiens of	ER GV chromosome	13 clone RP.
<u>ID NO:1)</u>	Active site I: PBP: 35 AA's upstreamdownstream from N-term	inus:	STTK (SEQ
ID NO:3)	NAALADase: 38 AA's upstreamdownstream from	n N-terminus	: STQK_(SEQ
<u> </u>	emb AL162372.6:	STQ-	
motif: SFG	Active site II: PBP: 57 AA's upstreamdownstream from STTK (SEQ ID NO:1) SGC, SGN, or SAN NAALADase: 59 AA's upstreamdownstream from STQK (SEQ ID NO:3)		
	emb AL162372.6:	SFG	
	Active site III: PBP:111 AA's upstreamdownstream from SGC m NAALADase: 110 AA's upstreamdownstream fro emb AL162372.6:	otif: m SFG motif KLG	. KTG : KLG
<u>ID NO:2)</u>	Active site IV: PBP:41 AA's upstreamdownstream from SGC mo	tif:	ENKD <u>(SEQ</u>

ID NO.4)	NAALADase: 41 AA's upstreamdownstream from SFG motif: ERGV (SEQ		
<u>ID NO:4)</u>	emb AL162372.6 ER GV 6) gb AC024234.5 AC024234 Homo sapiens chromosome 11 clone RP1.		
<u>ID NO:1)</u> <u>ID NO:3)</u>	Active site I: PBP: 35 AA's upstreamdownstream from N-terminus:		
	NAALADase: 38 AA's upstreamdownstream from N-terminus: STQK (SEQ		
	gb AC024234.5 AC024234: STQ-		
	Active site II:		
motif:	PBP: 57 AA's upstreamdownstream from STTK (SEQ ID NO:1) SGC, SGN, or SAN		
motif: SFG	NAALADase: 59 AA's upstreamdownstream from STQK (SEQ ID NO:3)		
	gb AC024234.5 AC024234: SFG		
	Active site III: PBP:111 AA's upstreamdownstream from SGC motif: KTG NAALADase: 110 AA's upstreamdownstream from SFG motif: KLG gb AC024234.5 AC024234: KLG		
<u>ID NO:2)</u>	Active site IV: PBP:41 AA's upstreamdownstream from SGC motif: ENKD (SEQ)		
	NAALADase: 41 AA's upstreamdownstream from SFG motif: ERGV_(SEQ		
. <u>ID NO:4)</u>	gb AC024234.5 AC024234 ER GV 7) dbj AP002369.1 AP002369 Homo sapiens chromosome 11 clone RP		
<u>ID NO:1)</u> <u>ID NO:3)</u>	Active site I: PBP: 35 AA's upstreamdownstream from N-terminus: STTK (SEQ)		
	NAALADase: 38 AA's upstreamdownstream from N-terminus: STQK (SEQ		
	dbj AP002369.1: STQ-		
motif:	Active site II: PBP: 57 AA's upstreamdownstream from STTK (SEQ ID NO:1) SGC, SGN, or SAN		
	NAALADase: 59 AA's upstreamdownstream from STQK (SEQ ID NO:3)		
	dbj AP002369.1: SFG		
	Active site III:		

Active site IV:

PBP:41 AA's upstreamdownstream from SGC motif:..... ENKD (SEQ

ID NO:2)

NAALADase: 41 AA's upstreamdownstream from SFG motif: ERGV (SEQ

ID NO:4)

dbj|AP002369.1 ER GV

5. Please amend the paragraphs beginning on page 14, line 5 and ending on line 21, as follows:

Enhanced concentrations of drug substances, including NAALADase inhibitors in the brain, can also be achieved by co-administration with P-glycoprotein efflux inhibitors such as those described in U.S. Patent Numbers 5,889,007; 5,874,434; 5,654,304; 5,620,855; 5,643,909; and 5,591,715, the specifications of which patents are expressly incorporated herein by reference. Alternatively, β-lactam β-lactams antibiotic compounds useful in accordance with this invention, including penicillins, cephalosporins, penems, 1-oxa-1-dethia cephems, clavams, clavems, azetidinones, carbapenams, carbapenems, and carbacephems, can be administered alone or in combination with art-recognized β-lactamase inhibitors, which themselves may or may not be β-lactam compounds or compounds capable of exhibiting selective affinity for penicillin-binding proteins. Examples of β-lactamase inhibitors which can be used alone or in combination with other neuropeptidase inhibitors useful in accordance with this invention for treatment and/or prevention of cognitive or behavioral disorders are other β-lactam compounds which may or may not exhibit independent clinically significant antibacterial activity, such as clavulanic acid and thienamycin and analogs thereof, sulbactam, tazobactam, sultamicillin, and aztreonam and other monolactams.

6. Please amend the paragraphs beginning on page 34, line 22 and ending on page 35, line 4, as follows:

In one preferred embodiment of the present invention the protease inhibitor is a compound of the formula:

wherein R is hydrogen, a salt forming group or an active ester forming group; R^1 is hydrogen or C_1 - C_4 alkoxy; T is C_1 - C_4 alkyl, halo (including ehlori, fluro, biomochloro, fluoro, bromo, and iodo), hydroxy, $O(C_1$ - C_4)alkyl, or - CH_2B wherein B is the residue of a nucleophile B:H, and aeyl-Acyl is the residue of an organic acid Aeyl-OHAcyl-OH.

7. Please amend the paragraphs beginning on page 36, line 5 and ending on line 18, as follows:

Suitable pharmaceutically acceptable salts of the carboxy group of the above identified β-lactam antibiotics or glutamate derivatives or analogs include metal salts, e.g. aluminum, alkali metal salts such as sodium or potassium, alkaline earth metal salts such as calcium or magnesium, and ammonium or substituted ammonium salts, for example those with lower alkylamines such as triethylamine, hydroxy-lower alkylamines such as 2-hydroxyethylamine, bis-(2-hydroxyethyl)amine or tris-(2-hydroxyethyl)amine, cycloalkylamines such as dicyclohexylamine, or with procaine, dibenzylamine, N,N-dibenzylethylenediamine, 1-ephenamine, N-methylmorpholine, ethylpiperidineN-ethylpiperidine, N-benzyl-β-phenethylamine, dehydroabietylamine, N-N²-bisdehydro-abietylamine, ethylenediamine, or bases of te-bases of the pyridine type such as pyridine, collidine or quinoline, or other amines which have been used to form salts with known penicillins and cephalosporins. Other useful salts include the lithium salt and silver salt. Salts within compounds of formula (I), may be prepared by salt exchange in conventional manner.

8. Please amend the paragraphs beginning on page 69, line 5 and ending on line 15, as follows:

These data indicate that the antiaggressive effect of the beta-lactam antibiotic Mox may be extended to include the beta-lactam ampicillin. Off all of the Of all of the antibiotic tested, Mox has the greatest penetrability into the CNS. Patents given 2.0 g of Mox IV show cerebrospinal fluid levels of drug around 30 μ g/ml. The ratio of CSF to serum levels of Mox is ca. 15-20%. It is estimated that the serum concentration of Mox in 140 g hamster

given an IP injection of 14 µg of drug is 0.1 ng/ml. This would be reflected by a CSF concentration of 15 ng/ml or brain levels of Mox approximating 30 nM. These levels would certainly be in range to interact effectively with neuropeptide receptors most of which have binding affinities in the nanomolar range. Interaction with the classical neurotransmitters would be less likely because these receptors have Kd's in the micro and millimolar range.

9. Please amend the paragraphs beginning on page 90, line 1 and ending on line 11, as follows:

Active site I:

35 AA's upstreamdownstream from N-terminus: STTK (SEQ ID NO:1)

Active site II:

57 AA's upstreamdownstream from STTK (SEQ ID NO:1) motif: SGC, SGN, or SAN

Active site III:

111 AA's upstreamdownstream from SGC motif: KTG

Active site IV:

41 AA's upstreamdownstream from SGC motif: ENKD (SEQ ID NO:2)

10. Please amend the paragraphs beginning on page 90, line 25 and ending on page 91, line 3, as follows:

Active site I:

Beta-lactamase: 35 AA's upstreamdownstream from N-terminus: STTK_(SEQ)

<u>ID NO:1)</u>

NAALADase: 38 AA's <u>upstreamdownstream</u> from N-terminus: STQK (SEQ ID NO:3)

Active site II:

Beta-lactamase: 57 AA's upstreamdownstream from STTK (SEQ ID NO:1)

motif: SGC, SGN, or SAN

NAALADase: 59 AA's upstreamdownstream from STQK (SEQ ID NO:3)

motif: SFG

Active site III:

Beta-lactamase: 111 AA's <u>upstreamdownstream</u> from SGC motif: KTG NAALADase: 110 AA's <u>upstreamdownstream</u> from SFG motif: KLG

Active site IV:

Beta-lactamase: 41 AA's upstreamdownstream from SGC motif: ENKD (SEQ

ID NO:2)

NAALADase: 41 AA's upstreamdownstream from SFG motif: ERGV (SEQ ID NO:4)

Amendments to the Specification under 37 C.F.R. § 1.121(B)(1)

Please amend the abstract as follows:

Abstract of the Disclosure

Administration of β-Lactam compounds, including β-lactam antibiotics and β-lactamase inhibitors provides of inhibitors of certain bacterial peptidase have been found to provide significant neurotropic effects in warm-blooded vertebrates evidenced *inter alia* by anxiolytic and anti-aggressive behavior modification and enhanced cognition believed to be mediated by inhibition of neurogenic NAALADase and related enzyme activity. β-Lactam antibiotics and β-lactamase inhibitors have been found to exhibit potent NAALADase inhibition, and those compounds with blood brain barrier transport are effective inhibitors of neurogenic NAALADase with significant neuro-therapeutic effects. β-Lactam compounds are useful for treatment of numerous disease states associated with glutamate abnormalities. Therapeutic methods for using such compounds and their pharmaceutical formulations are described.